

ELECTRONIC APPENDIX

Origin, adaptive radiation, and
diversification of the Hawaiian
lobeliads (Asterales:
Campanulaceae)

Thomas J. Givnish, Kendra C. Millam, Austin R. Mast, Thomas B. Patterson, Terra J. Theim, Andrew L. Hipp, Jillian M. Henss,
James F. Smith, Kenneth R. Wood, and Kenneth J. Sytsma

Phylogenetic analyses

Sequence data – We derived a phylogeny for the Hawaiian lobeliads using sequence data for *rpl16*, ca. 350 nucleotides at the 5' end of *rbcL*, and five rapidly evolving intergenic spacers (*psbA-trnH*, *trnL-trnF*, *trnT-trnL*, *trnV-trnK*, *atpB-rbcL*) from the chloroplast genome for 23 species representing all endemic Hawaiian genera and both endemic sections of *Lobelia*, and 15 species representing all groups previously proposed as close relatives or potential ancestors (Table A1). We amplified and sequenced each DNA segment except *trnV-trnK* using standard techniques (Golenberg et al. 1990; Taberlet et al. 1991; Manen et al. 1994; Jordan et al. 1996; Sang et al. 1997). Due to a series of inversions in the plastid genome, *trnV* and *trnK* adjoin each other and bracket a *trnV-trnK* intergenic spacer in giant woody *Lobelia* species and their relatives (Knox et al. 1993). We therefore designed the following primers to amplify and sequence this spacer: **KM-trnV** (CTATGAACTTAACGGTGTAT) and **KM-trnK** (GGAGAGGTTGTTACTT). We amplified *trnV-trnK* using 25 µL reactions containing 25 ng genomic DNA, 75 mM Tris-HCl pH 8.5, 1.5 mM MgCl₂, 20 mM (NH₄)₂SO₄, 0.1% Tween 20®, 0.8 mM spermidine, 0.2 mM dNTPs, 20 pmol of each primer, and 0.6 units GeneChoice *Taq* polymerase. Amplification used an initial denaturation for 5 min at 95°C, followed by 32 cycles of 30 s at 95°C, 60 s annealing at 50°C, and 90 s extension at 72°C, followed by a final extension step of 7 min at 72°C.

All PCR was performed on an MJ Research PTC-200 thermocycler. PCR products were purified using AMPure® (Agencourt Bioscience, Beverly, MA) and cycle-sequenced using ABI Prism® BigDye TM Terminator v. 3.1 (Applied Biosystems, Foster City, CA); dye-terminators were removed using CleanSEQ™ (Agencourt Bioscience). Sequences were run on ABI 377 or ABI 3100 automated sequencers, obtaining forward and reverse strands in all cases. Trace files were edited and aligned using Sequencher v. 3.0 (Gene Codes, Ann Arbor, MI).

A total of 4287 aligned bases were included in the analysis. Individual insertion/deletion events (indels) were treated as unweighted characters and scored in such a way as to minimize the number of additional evolutionary events (Baum et al. 1994). The 120 indels detected were easy to align in almost all cases, given their general restriction to small sets of taxa. Regions with

ambiguous alignments were excluded from analysis. All new sequences were uploaded to GenBank and accession numbers obtained (**Table A2**). Nomenclature follows Wagner et al. (1999) and the International Plant Name Index (<http://www.ipni.org>). An aligned data matrix is available upon request from the senior author.

Ingroup analysis – We evaluated evolutionary relationships using maximum parsimony (MP) and maximum likelihood (ML) as implemented in PAUP* 4.0b8 (Swofford 2002) and Bayesian analysis (BA) as implemented in MrBayes 3.1.2 (Ronquist et al. 2005), employing *Lobelia cardinalis* and *L. vivaldii* as outgroups. Indels – which provide several crucial informative characters for the Hawaiian clade and other groups – were only included in the MP analysis due to the difficulty of modeling indel characters under BA and the current impossibility of doing so in ML. The MP analysis gave nucleotide and indel characters equal weights. One thousand replicate searches were initiated with random starting trees and run to completion using TBR branch-swapping while retaining multiple trees. Two shortest trees were obtained, in both of which the Hawaiian lobeliads formed a clade sister to the African taxa; together these two groups were sister to the other woody lobeliads from the Pacific Basin. Jackknife support for each node was evaluated using 500 replicate resamplings of the data set and full heuristic searches using TBR branch-swapping and random branch addition. The parsimony-jackknife tree arising from these data (Farris et al. 1996) is identical to the MP tree preserving the monophyly of *Cyanea* (congruent with the well-supported results of Givnish et al. 1995). As expected from their residence in the same non-recombinant genome, nucleotide and indel characters showed no significance difference ($P > 0.62$) in phylogenetic structure based on the ILD test (Farris et al. 1994), which we implemented using 100 resamplings in PAUP*. The Hawaiian taxa are monophyletic in all unweighted trees for the nucleotide, indel, and combined data.

ML analyses were conducted on the nucleotide data only. ModelTest (Posada and Crandall 1998) was used to identify the model of sequence evolution that best fit the data. The best-fit model (TVM + G, with rate settings of 1.0140, 0.9568, 0.1276, 0.4526, and 0.9568, respectively, $N_{st} = 6$, and a gamma shape parameter of 0.7784) identified one most likely tree, identical to the

selected MP tree except that *Isotoma* forms a trichotomy with *Burmeistera-Centropogon* and *Lobelia excelsa* at the base of the tree. Bayesian analyses employed 4 independent runs using $N_{st} = 6$, ratio = invgamma, $N_{chains} = 4$ (3 heated chains, 1 cold), a run of 2 million generations, sample frequency = 100, and a burn-in of 5,000 (25% of 20,000 sampled generations). BA produced one tree (**Fig. A1**), identical in topology to the ML tree. The Hawaiian clade – together with all but five clades overall – had an *a posteriori* support of 100%; the sister relationship of the Hawaiians to the African clade was 96% (**Fig. A1**).

Outgroup analysis – We identified *Lobelia cardinalis* and *L. vivaldii* as suitable outgroups for polarizing the ingroup analysis based on two lines of evidence. First, Knox et al. (1993) inferred sequential inversions of the plastid genome in several lobeliads and used them to argue that, among 18 taxa sampled, *Lobelia cardinalis* was sister to a clade of 13 woody lobeliads from various tropical montane regions, including two species of *Lobelia* from Hawaii. However, several critical taxa – including *Pratia borneensis*, woody Caribbean taxa, and the fleshy-fruited Hawaiian genera – were not included in this study. Second, we sequenced *rbcL* for a stratified subset of the ingroup taxa, and downloaded sequences from GenBank for representatives of most families of the core campanulids, including the orders Asterales, Apiales, Dipsacales, and associated unplaced families (**Table A3**; nomenclature follows APG II 2003 and Bremer et al. 2004). These data yielded 86 shortest trees under codon-weighted parsimony (Albert et al. 1993), using *Arabidopsis* as a rosid outgroup and constraining Asteraceae and Calyceraceae to be sister to each other (Bremer et al. 2004). The strict consensus of the 86 shortest trees yielded a well-resolved phylogeny (**Fig. A2**).

This analysis showed that *Pratia borneensis* – proposed as a possible sister-group to the fleshy-fruited Hawaiian lobeliad genera *Clermontia*, *Cyanea*, and *Delissea* by Lammers (1990) – is only distantly related to the Hawaiian taxa. *Pratia* was therefore excluded from the ingroup analysis; sequences of rapidly evolving intergenic spacers for *Pratia*, not surprisingly, were difficult to align with those of the other taxa. The *rbcL* tree indicated that *Lobelia cardinalis* (North America) and *L. vivaldii* (Caribbean) are sister to each other; together, these two species

form one element of an unresolved trichotomy with *Centropogon*-*Isotoma* and a clade consisting of the remaining ingroup taxa represented. This identified *L. cardinalis*-*L. vivaldii* as a suitable outgroup for polarizing the ingroup taxa, with the proviso that relationships among these two taxa, *Centropogon*-*Burmeistera*, and *Isotoma* are uncertain and using another outgroup might influence relationships among them. Based on this analysis, *rbcL* had little phylogenetic signal for resolving relationships among the very closely related ingroup taxa, so only a relatively variable portion of this gene (ca. 350 nt near the 5' end, immediately adjoining the *atpB-rbcL* spacer) was sequenced across the ingroups. Using *Isotoma* as an outgroup in the MP ingroup analysis simply exchanges its position with that of *L. cardinalis*-*L. vivaldii*.

Character-state evolution

Data on the occurrence of fleshy vs. capsular fruits, terminal vs. axillary inflorescences, woody vs. herbaceous habit, and likely pollination agent of extant lobeliads were drawn from the literature (Wimmer 1953; Mabberly 1974, 1975; Lammers and Freeman 1986; Lammers 1989, 1990; Knox 1993; Knox et al. 1993; Givnish et al. 1994, 1995; Givnish 1998; Knox and Palmer 1998) and personal observations. We inferred ancestral character-states using parsimony, employing MacClade 4.0 (Maddison and Maddison 2001). Accelerated transformation was used to minimize the number of convergent gains of particular character-states. We overlaid character-states on the MP tree consistent with the monophyly of *Cyanea* and with the topology of the parsimony-jackknife tree, and with that of the ML and BA trees with the exception of *Isotoma* (**Fig. 2** in the text). *Lobelia erinus* and *Pratia borneensis* were appended to the bottom of the overlay tree, based on their position in the *rbcL* tree (**Fig. A2**).

We overlaid habitat-type and elevational range on the lobeliad phylogeny in similar fashion. Habitat-type was atomized as (0) rain- and cloud-forest gaps/ canopies; (1) rain- and cloud-forest understories; (2) mesic and dry forests; (3) cliffs and rocky outcrops; (4) alpine bogs and subalpine openings; (5) temperate meadows; (6) dry coastal scrub; and (7) deserts. Elevational range was classified as (0) low (< 400 m); (1) montane (> 400 m but below treeline); and (2) alpine/subalpine (at or above tree-line determined by elevation and/or drainage).

Sea cliffs and high-elevation bogs are late-developing features in the lifetime of individual islands (Carlquist 1970; Clague 1996), and that lava flows are wholly unlike recent lava flows at the same elevation in attaining far higher temperatures, and often less rainfall. It should also be noted that, once the flora has arrived, under rainy conditions on Hawaii a tall forest can develop in ca. 140 years on new lava flows (Aplet et al. 1998).

Chronological calibration of the molecular phylogeny

Nucleotides evolve in a significantly non-clocklike fashion in the ingroup tree ($P < 0.05$ by the Hasegawa et al. 1985 test). We therefore calibrated the molecular phylogeny using a rate-smoothed model and two alternative sets of calibration points, as follows.

Bottom-up approach: To establish a chronology for the origins of the Hawaiian clade and related groups, we used the computer program *r8s* (Sanderson 2002) to transform each of the 86 shortest outgroup trees (see above) using cross-verified penalized likelihood. After pruning the outgroup *Arabidopsis*, we calibrated branch lengths (under Wagner parsimony, with accelerated transformation) by fixing the ages of five internal nodes with five well-documented fossil asterids described by Bremer et al. (2004): (1) *Hironoia* (Cornaceae) at 88 Mya; (2) *Eurya* (Pentaphylaceae/Ternstroemiaceae) at 86 Mya; (3) *Saurauia* (Actinidiaceae) at 89 Mya; (4) *Ilex* (Aquifoliaceae) at 70 Mya; and (5) *Acanthopanax/Aralia* (Araliaceae) at 70 Mya. Our taxon sampling exactly matched that of Bremer et al. (2004) around these nodes to permit the same placement of fossils and dates; we also followed Bremer et al. (2004) in fixing the asterid root at 128 Mya.

Penalized likelihood (PL) averages local differences in the rate of DNA evolution on different branches, taking into account the topology of branching. PL differs from non-parametric rate-smoothing (NPRS) (Sanderson 1997) in assigning a penalty for excessively rapid or frequent changes in evolutionary rate among branches, based on a smoothness parameter. If the smoothness parameter is large, then PL approaches a clock-like model of molecular evolution; if the smoothness parameter is small, then PL approaches NPRS. We employed the cross-verification algorithm in *r8s* to find the optimal value of the smoothness parameter,

minimizing the sum of the squared deviations between observed and expected branch lengths derived through jackknifing each individual branch (Sanderson 2002). The smoothness parameter was varied from 10^0 to 10^3 in steps of 0.25 in the exponent; a value of $10^3 = 1000$ was found to be optimal for the outgroup tree. Cross-verified PL using all 86 trees identified two key dates on the outgroup tree: divergence of the Hawaiian crown group 13.38 ± 2.56 My ago (range: 8.33 – 19.85 My), and divergence of the *Lobelia cardinalis*-*L. vivaldii* lineage from that of the remaining ingroup taxa 22.65 ± 2.54 My ago (range: 18.22 – 28.16 My) (**Fig. A2**).

We used the two mean dates for the Hawaiian crown group (13.38 My) and divergence of *L. cardinalis*-*L. vivaldii* from other ingroup taxa (22.65 My) as fixed set points to calibrate the ingroup tree using cross-verified PL and MP branch lengths. The best smoothness parameter was 3.98 for the bottom-up analysis for the complete data set, and 1.00 for the top-down analysis. We used the average of these values (2.51) for bootstrapped analyses in order to apply a comparable approach to both; chronograms with smoothness parameters set between 1 and 1000 differed very little. We estimated two components of variation for each node date: SD_c = standard deviation of node age in the internal tree based on variation of calibration dates among external trees arising from 100 random bootstrappings of the external data, examining only the single most likely tree arising from the ingroup data; and SD_b = standard deviation of node age based on variation among 100 random resamplings of the ingroup data, fixing the two calibration ages imported from the external tree. Bootstrap resamplings were conducted using Seqboot in PhyloP 3.65 (Felsenstein 2004). The single best tree from the original ingroup data set was then saved in PAUP* with branch lengths derived from each bootstrap resampling. These trees, identical in topology but differing in branch lengths, were then converted to ultrametric form in r8s using the mean dates for the Hawaiian crown group and *L. cardinalis*-*L. vivaldii* node. Given that variations about mean node age due to calibration dates and to bootstrap resamplings are, by definition, independent random variables, the total standard deviation about each node age is equal to the hypotenuse of the two component standard deviations, $SD_{tot} = (SD_c^2 + SD_b^2)^{0.5}$.

Calculation of the mean \pm s.d. time *between* the colonization of Hawaii and a particular phylogenetic event was based on the difference between these dates in each bootstrap iteration. This “matched” comparison often results in standard deviations of date differences substantially less than the standard deviation about either date, because much of the variation in dates among bootstrap resamplings does not greatly increase the interval between dates in each resampling.

Using this approach, we inferred that the stem group of the Hawaiian clade arose 13.6 ± 3.11 My ago, and that clades adapted to wet-forest interiors (*Cyanea*), wet-forest gaps (*Clermontia*), sea cliffs (*Brighamia*), mesic forests and scrub (*Delissea*), and a variety of other open habitats (*Lobelia* sect. *Galeatella*, *Lobelia* sect. *Revolutella*, *Trematolobelgia*) had diverged by 9.01 ± 1.86 My ago (Fig. 4 in the text), within 4.37 ± 0.52 My of initial colonization. The montane-bog lineage (*Lobelia* sect. *Galeatella*) diverged from *Trematolobelgia* 6.98 ± 1.40 My ago, more than 2 My before Kaua`i emerged from the Pacific; extant species of *Lobelia* sect. *Galeatella* appear to have begun diverging from each other only in the last 1.34 ± 0.50 My (Fig. 4 in the text). SD_b , SD_c , and SD_{tot} rose, then fell toward the present (Fig. A3).

Top-down approach: We calibrated the ingroup phylogeny using the geological ages of the Hawaiian islands to which individual species were restricted. This approach assumes that species would invade an ecologically unsaturated island soon after it emerged from the Pacific (Givnish et al. 1995; Schneider et al. 2005). The following nodes were set equal to 4.7 My (estimated age of Kaua`i [Price & Clague 2004]), based on that node involving the divergence of a Kaua`i species from a species (or clade) restricted to younger islands: (a) *Clermontia fauriei* (K) vs. other *Clermontia* species; (b) *Cyanea leptostegia* (K) vs. *Cyanea coriacea* (K) (Givnish et al. 1995 found that both of these species were sister to a clade restricted to younger islands); (c) *Delissea rhytidosperma* (K) vs. *Delissea subcordata*; (d) *Brighamia insignis* (K) vs. *Brighamia rockii*; (e) *Trematolobelgia kauaiensis* (K) vs. *Trematolobelgia macrostachys*; and (f) *Lobelia gloria-montis* vs. *L. kauensis* (K) + *L. villosa* (K). We set the split between *Lobelia niihauensis* (N, K) vs. *L. hypoleuca* and *L. yuccoides* equal to 5.2 My, the estimated age of Ni`ihau. The divergence of *Cyanea acuminata* (O) vs. *Cyanea pilosa* + *Cyanea floribunda* was set equal to 3.0 My, the age of O`ahu. We

set the split between the last two species, both endemic to Hawai`i, equal to 0.6 My, the estimated age of the Big Island. We constrained the basal node of the ingroup phylogeny to be no more than 22.65 Mya, equal to its age based on the campanulid analysis (see above). Ages were again estimated using cross-verified penalized likelihood, as implemented in *r8s*, using calibration dates from each of the 86 shortest outgroup trees to estimate SD_c and bootstrap resamplings of the ingroup data to estimate SD_b (see above). This procedure yielded a stem-group age of the Hawaiian lobeliads of 13.0 ± 1.00 My (**Fig. 4B** in the text). This analysis also implied that the forest and non-forest lineages diverged within 0.30 ± 0.15 My of initial colonization, and that all of the genera/endemic sections had diverged from each other within 3.55 ± 0.72 My of colonization. SD_b rose, then fell toward the present, while SD_c and SD_{tot} fell monotonically in the top-down analysis (**Fig. A4**). The non-bootstrapped ages for both calibrations show remarkable agreement: Top-down age = $0.921 \bullet$ bottom-up age + 1.34, $r^2 = 0.966$, $P < 0.0001$ for 33 d.f. (excluding the 22.65 My set-point held in common between the two analyses) (**Fig. A5**).

Determinants of diversity in the Hawaiian lobeliads

We compiled data on the island distribution and elevational range of all currently recognized species of endemic Hawaiian lobeliads from Lammers (1990, 1996, 1998, 2004) and Lammers and Proctor (1994); additional data on certain rare species were provided by David Lorence, Hank Oppenheimer, Fern Duvall, and Clyde Imada. Mean elevation of each lobeliad species was taken to be the average of the minimum and maximum elevations reported. Similarly, for each species of *Cyanea*, the mean length of the floral tube was calculated as the average of the minimum and maximum values reported. For each of the four major islands (Kaua`i, O`ahu, Maui, Hawai`i), each species was plotted by mean elevation x mean floral tube length (**Table A4; Fig. 5** in the text).

We tallied the mean number of islands occupied by each species in each genus, and then calculated the mean \pm s.d. of this index for genera having different mechanisms of seed dispersal (see text). We also compiled the number of species from each genus on each of the

eight large islands (Ni`ihau to Hawai`i; **Table A5**). Island age, elevation, and area (Walker 1990; Clague 1996; Price & Wagner 2004) are also summarized in **Table A5**.

To assess the ecological and evolutionary determinants of species richness in *Cyanea* on different islands, we conducted a backwards-elimination multiple regression of $\ln(1 + \text{species number})$ against $\ln \text{age}$, $\ln \text{elevation}$, and $\ln \text{area}$. All statistical calculations were performed using R (<http://www.r-project.org/>). Elevation was transformed to reflect the range of elevations actually invaded by *Cyanea*: $\epsilon = \max(0, [\min(E, 2000) - 200])$ = the minimum of actual island elevation (E) and 2000 m (the maximum mean elevation of all but one *Cyanea* species), reduced by 200 m (the minimum mean elevation of all but two species) and made non-negative. We would expect that all three factors should have a positive effect on species number, as a consequence of increased time for speciation, increased habitat diversity for ecological partitioning (see **Fig. 5**), and increased opportunity for geographic speciation and/or decreased chances of extinction due to larger population sizes, respectively. With all islands included, only elevation (ϵ) remained as a significant factor influencing the number of *Cyanea* species (S):

$$S = 6.39 \times 10^{-4} \epsilon^{1.38} - 1$$

($r^2 = 0.89$, $P < 0.001$ for 6 d.f.). Hawai`i is an outlier of this relationship, with only 65% of the species expected (12 observed vs. 18.4 expected). When Hawai`i is excluded, backwards-elimination multiple regression yields a highly significant model across all older islands, with *Cyanea* species number S increasing with both island elevation ϵ and area A:

$$\ln(1+S) = 0.620 \ln \epsilon + 0.761 \ln A - 7.12$$

($r^2 = 0.995$, $P < 0.01$ for each variable with 4 d.f., $P < 5 \times 10^{-5}$ overall). Hawai`i is the only outlier in this model and deviates quite substantially from it, having but one-eighth the number of *Cyanea* species expected (12 vs. 95.6; see **Table A6**). Given that (1) essentially all the variance in *Cyanea* species number is accounted for in this model (or in the simpler model based solely on elevation); that (2) island age is not a significant factor in either model (i.e., for islands > 1.2 My old); and that (3) the number of species on Hawai`i (0.6 My) is between one-half and one-eighth its expected saturated level, we conclude that full ecological saturation was achieved most

recently on Maui and Lana`i (1.5 My) and that completion of community assembly – involving speciation and the partitioning of elevation and pollinator bill length – requires more than 0.6 My and less than 1.5 My. The number of other native lobeliad species is strongly correlated with the number of *Cyanea* species ($r = 0.82$, $P < 0.02$ for 6 d.f.).

Net rate of diversification

We calculated the net rate of species diversification in *Cyanea* on individual islands using the formula $D = \ln (\# \text{ current species} / \# \text{ surviving colonist species}) / \text{age of island}$ (see Hughes & Eastwood 2006). Not surprisingly, this rate reaches its peak on Maui, the youngest island on which we have evidence suggesting ecological saturation. It would be highly misleading to calculate D as $\ln (\text{total number of species}) / \text{age of radiation}$ for *Cyanea* or the Hawaiian lobeliads as a whole, given that so many species restricted to single islands would have gone extinct over the past 13 My, based on the reduction of islands older than 5.2 My to mere pinnacles with no lobeliads, and ecological saturation on present-day islands older than Hawai`i (0.6 My old).

Overall species number in Hawaiian lobeliads vs. other clades of island plants

We compiled data on the number of species in the largest known clades of plants restricted to individual oceanic (i.e., non-raft, non-landbridge) islands or archipelagoes around the world, surveying the literature for phylogenetic studies of insular groups based on molecular data or careful morphological analysis. Within the diverse Hawaiian flora, the endemic lobeliads are by far the largest clade with 126 spp., followed by *Cyrtandra* (Rubiaceae) with 58 spp. (Cronk et al. 2005), the endemic Hawaiian mints (*Haplostachys-Phyllostegia-Stenogyne*, Lamiaceae) with 57 spp. (Lindqvist & Albert 2002) and *Schiedea* (Caryophyllaceae) with 32 spp. (Nepokroeff et al. 2005). All other known Hawaiian clades are substantially smaller (Baldwin 2003; Price and Wagner 2004); only *Melicope* (Rutaceae) with 47 spp. could potentially break into the top five, based on group size and expert views regarding the origins of Hawaiian plants based on morphological evidence (Carlquist 1974; Sakai et al. 1995). Only the small aspleniod fern genus *Diellia* (6 spp.) – with an apparent arrival ca. 24 Mya (Schneider et al. 2005) – has an inferred age greater than the lobeliads among the Hawaiian plant clades with chronologically calibrated

phylogenies; all others have inferred ages \leq 5.1 My (Price and Wagner 2004). The high diversity of the Hawaiian lobeliads might reflect, in part, its early arrival in the Hawaiian chain via niche pre-emption, as argued by Carine et al. (2004), Silvertown (2004), and Silvertown et al. (2005) for elements of the Macaronesian flora (see contrary views by Herben et al. 2005 and Saunders and Gibson 2005). However, niche pre-emption seems likely to be less important than the effects of dispersal and habitat partitioning (see text) in *Cyanea* and the Hawaiian lobeliads generally, given the restriction of most species to individual islands, the rapid demise of older islands and (presumably) the species present on them, and the much smaller size of lineages (e.g., Hawaiian mints, silversword alliance) that invaded the current islands as they were formed, at the same time as they were invaded by the Hawaiian lobeliads.

In the Macaronesian archipelago, the largest clades are the *Aeonium* alliance (Crassulaceae) with 63 spp. (apparently the second largest clade restricted to any single truly oceanic island or archipelago, after the Hawaiian lobeliads); *Echium* (Boraginaceae) with 37 spp.; and the *Sonchus* alliance (Asteraceae) with 34 spp. (Bohle et al. 1996; Francisco-Ortega et al. 1996; Kim et al. 1996; Mes and t'Hart 1996; Mort et al. 2002; Silvertown 2004). After the Hawaiian lobeliads, the largest known group of plants derived from a single ancestor endemic to any single island or archipelago is the *Hebe* complex (*Hebe*, *Chionohebe*, *Parahēbe*, *Hebejeebie*, Plantaginaceae) in New Zealand with 124 species (Garnock-Jones 1993; Albach et al. 2004, 2005; New Zealand Plant Database at <http://nzflora.landcareresearch.co.nz/>). New Zealand, however, is an ancient continental raft with geological age and edaphic diversity greatly exceeding that of the Hawaiian chain and other true oceanic archipelagoes. A group of ca. 11 species from New Guinea is embedded within the 124-species New Zealand group (Albach et al. 2005). Perhaps the next largest group derived from a single ancestor on any single island/archipelago is the *Pouteria* complex (Sapotaceae), with ca. 80 spp. on New Caledonia (Bartish et al. 2005); New Caledonia, however, is another ancient, edaphically complex continental raft. Finally, it should be noted that there are several plant clades that occur on several archipelagoes and which each have more species than the Hawaiian lobeliads; examples include *Cyrtandra* (Gesneriaceae) with

ca. 600 species across the Pacific, with centers of diversity in and around New Guinea and the Philippines (Cronk et al. 2005); *Psychotria* (Rubiaceae), with several hundred Pacific species (Nepokroeff et al. 2003); and *Myrsine* (Myrsinaceae) with 150-200 species in the Pacific (Wagner et al. 1990). *Pittosporum* (Pittosporaceae) also has more than 100 species on Pacific islands (Gemmill et al. 2002). These widespread groups have numerous species scattered across numerous archipelagoes in the Pacific; presumably, in each lineage, vast geographic distances have combined with limited dispersal to produce rampant geographic speciation, reproducing at a much larger spatial scale the same kinds of processes hypothesized to drive high diversity in the Hawaiian lobeliads (see also Price and Wagner 2004).

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Figure legends

- A1.** Ingroup phylogeny derived using Bayesian analysis, based on all sequence data excluding the indels. *A posteriori* support values are shown in blue; unlabelled nodes had support values of 100%. The green box and red branches highlight the Hawaiian clade.
- A2.** Outgroup chronogram derived from one of the 86 shortest outgroup trees using cross-verified penalized likelihood and the fossil dates indicated. Nodes with greater than 50% bootstrap support are highlighted. Hollow arrowheads indicate nodes that collapse in the strict consensus tree. Dates used to calibrate the ingroup phylogeny are 13.38 My (average across all outgroup trees) for the crown group of the Hawaiian lobeliads (*) and 22.65 My (average across all outgroup trees) for the crown group subtended by the Hawaiian lobeliads and *Lobelia cardinalis-L. vivaldii* (**).
- A3.** SD_b , SD_c , and SD_{tot} as a function of node age (estimated using the average calibration set-points from the outgroup phylogeny) in the bottom-up analysis. Constrained nodes were excluded from the analysis.
- A4.** SD_b , SD_c , and SD_{tot} as a function of node age (estimated using the average calibration set-points from the outgroup phylogeny) in the top-down analysis. Constrained nodes were excluded from the analysis.
- A5.** Relationship between non-bootstrapped ages for both calibrations of the ingroup chronogram: Top-down age = $0.921 \bullet$ bottom-up age + 1.34, $r^2 = 0.966$, $P < 0.0001$ for 33 d.f.

Figure A1

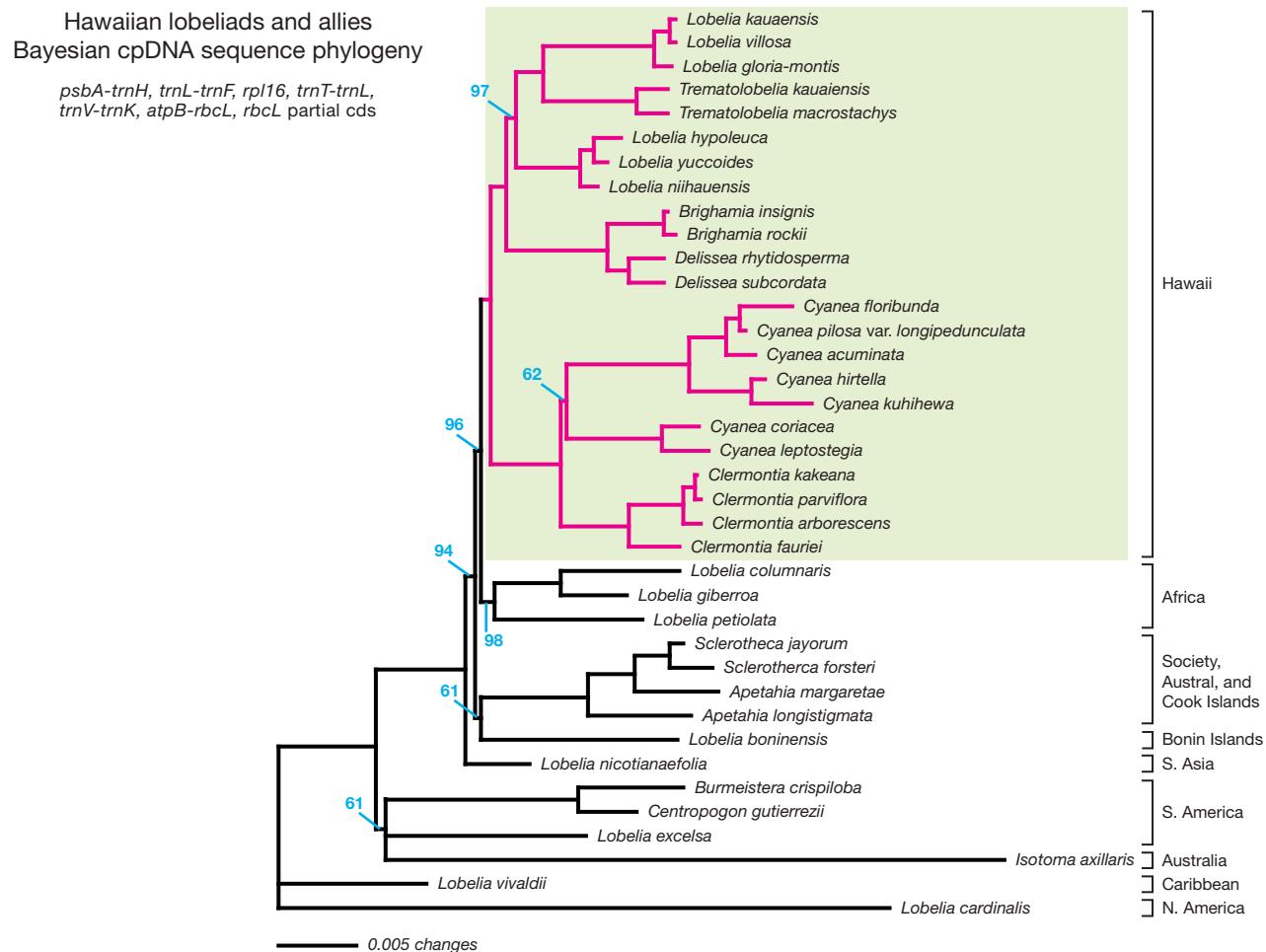


Figure A2



Figure A3

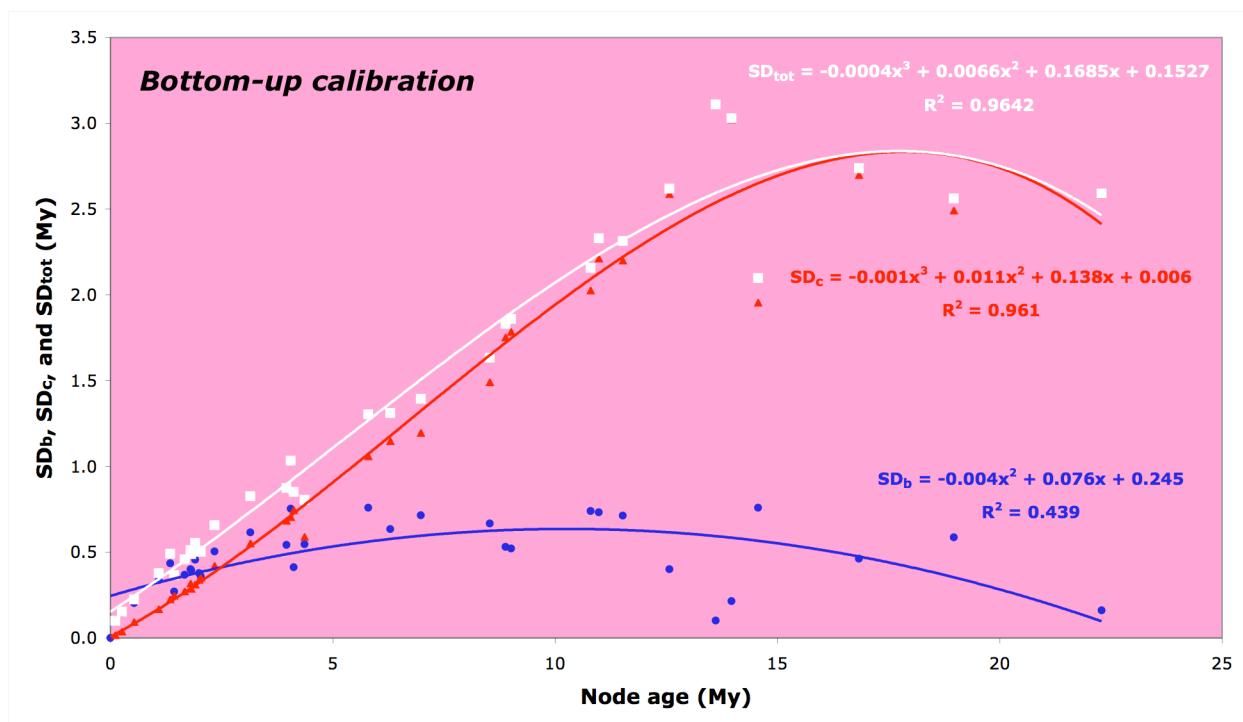


Figure A4

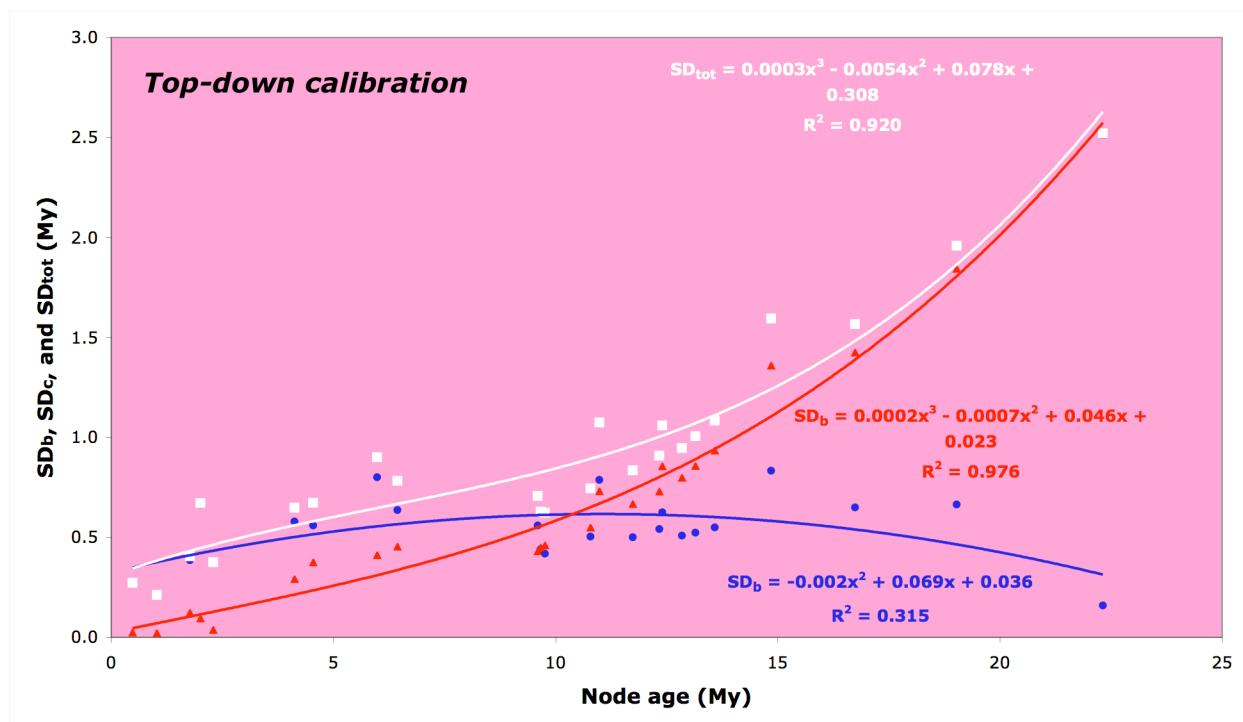


Figure A5

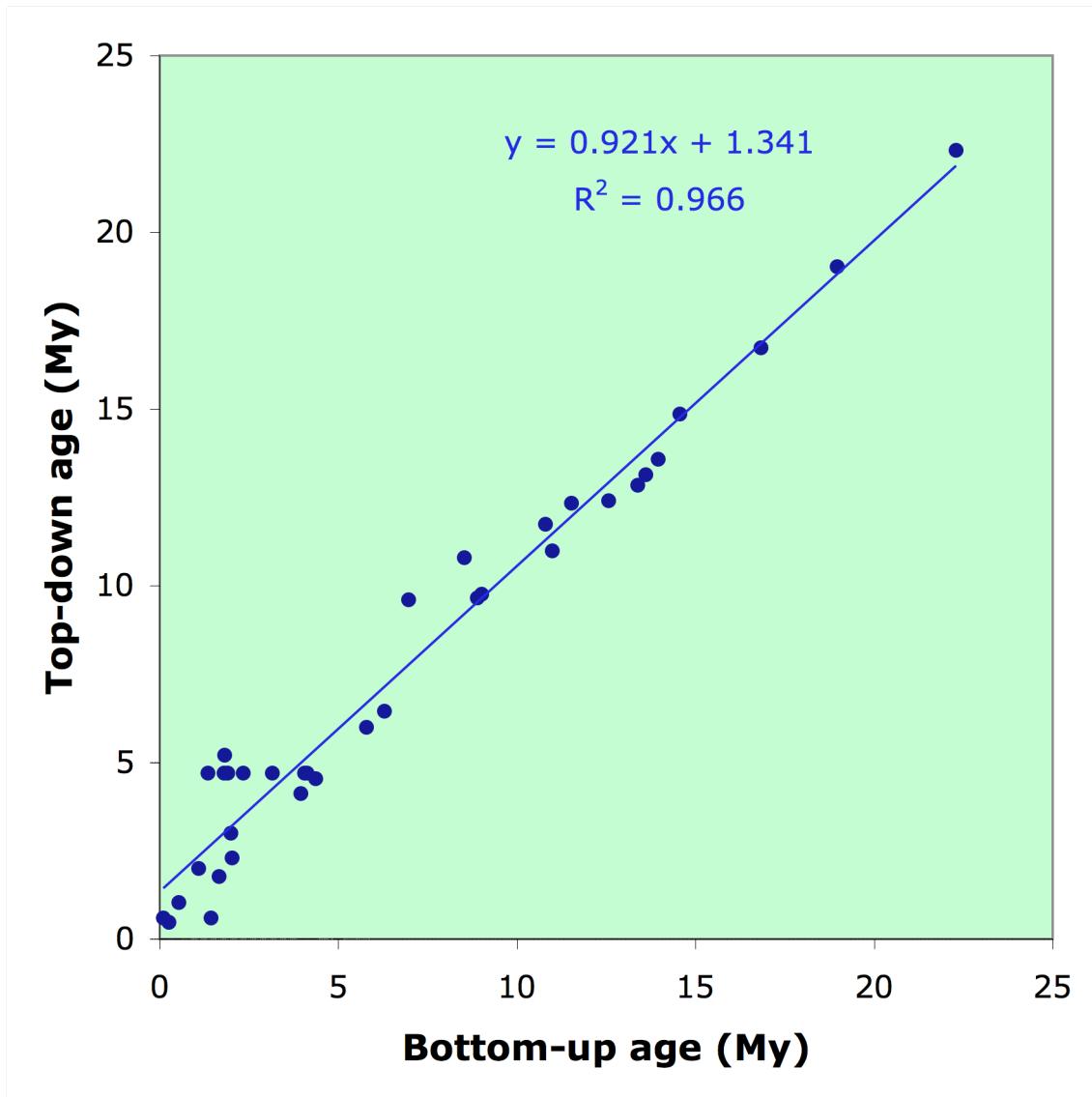


Table A1. Putative relatives/ancestors of the Hawaiian lobeliads advanced on morphological grounds.

Hawaiian taxon	# spp.	Habitat and growth form	Proposed relatives	Source area	Citations
Wind-dispersed taxa with dry capsular fruits:					
<i>Brighamia</i>	2	Sea-cliff succulents	<i>Sclerotheca/Apetahia</i>	Rarotonga, Society Islands, Austral Islands, Marquesas	Rock 1919; Lammers 1989
			<i>Isotoma</i> sensu lato	Australia, West Indies, Society Islands	Rock 1919; Degener 1937; Carlquist 1969; Lammers 1989
			<i>Delissea</i>	Hawaii	Givnish et al. 1995; Buss et al. 2001
<i>Lobelia</i> sect. <i>Galeatella</i> ^a	4	Montane bog and grassland rosette shrubs	<i>Lobelia organensis</i> and allies*	Brazil	Mabberley 1974, 1975; Lammers 1999
			<i>L. boninensis</i>	Bonin Islands	Koidzumi 1914; Lammers 1999
			<i>L. columnaris</i> , <i>L. giberroa</i> , <i>L. petiolata</i> and allies*	East and West African Highlands	Mabberley 1975; Lammers 1999
			<i>L. excelsa</i> and allies [§]	Southern South America	Wimmer 1953; Mabberley 1974, 1975
<i>Lobelia</i> sect. <i>Revolutella</i> ^b	9	Cliff and rock-wall rosette shrubs	<i>Lobelia nicotianaefolia</i> and allies†	South Asia (India to Philippines)	Skottsberg 1928; Mabberley 1974, 1975; Murata 1995; Lammers 1999
			<i>L. excelsa</i> and allies [§]	Southern South America	Wimmer 1953; Mabberley 1974, 1975
<i>Trematolobelia</i>	2	Subalpine wet-forest treelets	<i>Sclerotheca/Apetahia</i>	Rarotonga, Society Islands, Austral Islands, Marquesas	Wimmer 1953
			<i>Lobelia</i> sect. <i>Galeatella</i>	Hawaii	Mabberley 1974, 1975; Lammers 1999
			<i>Lobelia organensis</i>	Brazil	Mabberley 1974, 1975
Bird-dispersed taxa with baccate (fleshy) fruits:					
<i>Clermontia</i>	22	Mesic and wet forest-edge shrubs and trees	<i>Burmeistera/Centropogon</i>	Central and South America	Rock 1919; Brown 1921; Stone 1967; Carlquist 1970, 1974; Lammers 1999
<i>Cyanea</i>	76	Mesic and wet forest-interior trees, treelets, and vines			
<i>Delissea</i>	10	Dry scrub, mesic forest treelets		Borneo	Lammers 1999

**Lobelia* sect. *Rhynchopetalum* subsect. *Haynaldinae* E. Wimmer; †*Lobelia* sect. *Rhynchopetalum* subsect. *Nicotianifoliae* Mabberley, *Lobelia* subg. *Tupa* sect. *Colensoa* Murata; §*Lobelia* sect. *Tupa* subsect. *Eutupa* E. Wimmer; ^a*Galeatella* Degener & Degener (1974); ^b*Neowimmeria* Degener & Degener (1965);

Table A2. GenBank accession numbers for lobeliad taxa included in the ingroup phylogenetic analysis.

Taxon	Distribution	Collection/reference	<i>psbA-trnH</i>	<i>rpl16</i> intron	<i>trnL-trnF</i>	<i>trnT-trnL</i>	<i>trnV-trnK</i>	<i>atpB-rbcL</i> **
Hawaiian taxa								
<i>Brighamia insignis</i> A. Gray	Kaua`i	Givnish & Sytsma 3001, WIS	DQ272693	DQ285100	DQ285139	DQ285217	DQ285178	DQ285256
<i>Brighamia rockii</i> St. John	Moloka`i	Wood 0402, PTBG	DQ272694	DQ285101	DQ285140	DQ285218	DQ285179	DQ285257
<i>Clermontia arborescens</i> (H. Mann) Hillebr.	Moloka`i*	Smith, Sytsma, Givnish, Misaki 1162, WIS	DQ272695	DQ285102	DQ285141	DQ285219	DQ285180	DQ285258
<i>Clermontia fauriei</i> H. Lev	Kaua`i	Smith, Lorence, Flynn 1137, WIS	DQ272696	DQ285103	DQ285142	DQ285220	DQ285181	DQ285259
<i>Clermontia kakeana</i> Meyen	Maui*	Givnish & Sytsma 3003, WIS	DQ272697	DQ285104	DQ285143	DQ285221	DQ285182	DQ285260
<i>Clermontia parvifolia</i> Gaud. ex A. Gray	Hawai`i	Smith 2142, WIS	DQ272625	DQ285132	DQ285171	DQ285249	DQ285210	DQ285288
<i>Cyanea acuminata</i> (Gaud.) Hillebr.	O`ahu	Obata & Palmer 433, BISH	DQ272698	DQ285105	DQ285144	DQ285222	DQ285183	DQ285261
<i>Cyanea coriacea</i> (A. Gray) Hillebr.	Kaua`i	Flynn 3492, PTBG	DQ272699	DQ285106	DQ285145	DQ285223	DQ285184	DQ285262
<i>Cyanea floribunda</i> (F. Wimmer) Lammers	Hawai`i	Givnish 3105, WIS	DQ272727	DQ285134	DQ285173	DQ285251	DQ285212	DQ285290
<i>Cyanea hirtella</i> (H. Mann) Hillebr.	Kaua`i	Smith, Lorence, Flynn 1138, WIS	DQ272729	DQ285136	DQ285175	DQ285253	DQ285214	DQ285292
<i>Cyanea kuhihewa</i> Lammers	Kaua`i	Wood, Wichman, Perlman, Marr 0820, PTBG	DQ272731	DQ285138	DQ285177	DQ285255	DQ285216	DQ285294
<i>Cyanea leptostegia</i> A. Gray	Kaua`i	Smith, Lorence, Flynn 1135, WIS	DQ272726	DQ285133	DQ285172	DQ285250	DQ285211	DQ285289
<i>Cyanea pilosa</i> A. Gray, subsp. <i>longipedunculata</i>	Hawai`i	Givnish 3105, WIS	DQ272728	DQ285135	DQ285174	DQ285252	DQ285213	DQ285291
<i>Delissea rhytidosperma</i> H. Mann	Kaua`i	Lyon Arboretum, cultivated plant	DQ272700	DQ285107	DQ285146	DQ285224	DQ285185	DQ285263
<i>Delissea subcordata</i> Gaud.	O`ahu	Obata, Palmer, Rice, Maxwell 345, BISH	DQ272701	DQ285108	DQ285147	DQ285225	DQ285186	DQ285264
<i>Lobelia gloria-montis</i> [†] Rock	Maui*	Givnish 1008, WIS	DQ272702	DQ285109	DQ285148	DQ285226	DQ285187	DQ285265
<i>Lobelia hypoleuca</i> [§] Hillebr.	Oahu*	Givnish 1017, WIS	DQ272703	DQ285110	DQ285149	DQ285227	DQ285188	DQ285266
<i>Lobelia kauaensis</i> [†] (A. Gray) A. Heller	Kaua`i		DQ272704	DQ285111	DQ285150	DQ285228	DQ285189	DQ285267
<i>Lobelia niihauensis</i> [§] St. John	Kaua`i*	Smith 1133, WIS	DQ272705	DQ285112	DQ285151	DQ285229	DQ285190	DQ285268
<i>Lobelia villosa</i> [†] (Rock) St. John & Hosaka	Kaua`i	Wood 3672, PTBG	DQ272730	DQ285137	DQ285176	DQ285254	DQ285215	DQ285293
<i>Lobelia yuccoides</i> [§] Hillebr.	Kaua`i	Wood 3483, PTBG	DQ272706	DQ285113	DQ285152	DQ285230	DQ285191	DQ285269
<i>Trematolobelia kauaiensis</i> (Rock) Skottsb.	Kaua`i	Smith, Lorence, Flynn 1136, WIS	DQ272707	DQ285114	DQ285153	DQ285231	DQ285192	DQ285270
<i>Trematolobelia macrostachys</i> (Hook. & Arnott) A. Zahlbr.	Hawai`i*	Smith 2144, WIS	DQ272708	DQ285115	DQ285154	DQ285232	DQ285193	DQ285271
Non-Hawaiian taxa								
<i>Apetahia longistigmata</i> (F. Br.) E. Wimmer	Marquesas Islands	Wood 6480, PTBG	DQ272709	DQ285116	DQ285155	DQ285233	DQ285194	DQ285272
<i>Apetahia margaretae</i> (F. Br.) E. Wimmer	Rapa (Austral Islands)	Meyer 993, PAP	DQ272723	DQ285130	DQ285169	DQ285247	DQ285208	DQ285286
<i>Burmeistera crispiloba</i> A. Zahlbr.	Ecuador	Smith 1975, WIS	DQ272718	DQ285125	DQ285164	DQ285242	DQ285203	DQ285281

<i>Centropogon gutierrezii</i> E. Wimmer	Costa Rica	Iltis 30360, WIS	DQ272719	DQ285126	DQ285165	DQ285243	DQ285204	DQ285282
<i>Isotoma axillaris</i> Lindl.	Australia	Knox 2368, MICH	DQ272720	DQ285127	DQ285166	DQ285244	DQ285205	DQ285283
<i>Lobelia boninensis</i> Koidz.	Bonin Islands	S Kobayashi, s.n.	DQ272711	DQ285118	DQ285157	DQ285235	DQ285196	DQ285274
<i>Lobelia cardinalis</i> L.	North America	Givnish, field id	DQ272722	DQ285129	DQ285168	DQ285246	DQ285207	DQ285285
<i>Lobelia columnaris</i> Hook.	Western Africa	Hamilton, s.n., MICH	DQ272712	DQ285119	DQ285158	DQ285236	DQ285197	DQ285275
<i>Lobelia excelsa</i> Bonpl.	Chile	Lammers 6393, F	DQ272713	DQ285120	DQ285159	DQ285237	DQ285198	DQ285276
<i>Lobelia giberroa</i> Hemsl.	East Africa	Knox 118, MICH	DQ272714	DQ285121	DQ285160	DQ285238	DQ285199	DQ285277
<i>Lobelia nicotianaeifolia</i> Heyne ex Roem. & Schult.	India	Knox 2353, MICH	DQ272715	DQ285122	DQ285161	DQ285239	DQ285200	DQ285278
<i>Lobelia organensis</i> Gardn.	Brazil	Knox 90, MICH	DQ272716	DQ285123	DQ285162	DQ285240	DQ285201	DQ285279
<i>Lobelia petiolata</i> Hauman	Rwanda/Zaire	RBG accession 195.85.02600, K	DQ272717	DQ285124	DQ285163	DQ285241	DQ285202	DQ285280
<i>Lobelia vivaldii</i> Lammers & Proctor	Puerto Rico	G Kostermann, field ID	DQ272721	DQ285128	DQ285167	DQ285245	DQ285206	DQ285284
<i>Pratia borneensis</i> Hemsl.	Borneo	Givnish 4002., WIS						
<i>Sclerotheca forsteri</i> Drake	Moorea (Society Islands)	Meyer & Butaud 961, PAP	DQ272724	DQ285131	DQ285170	DQ285248	DQ285209	DQ285287
<i>Sclerotheca jayorum</i> J. Raynal	Society Islands	Berry 4630, MO	DQ272710	DQ285117	DQ285156	DQ285234	DQ285195	DQ285273

[†]*Lobelia* sect. *Galeatella*

[§]*Lobelia* sect. *Revolutella*

*Taxon occurs on other islands in the Hawaiian chain

**Includes ca. 350 bp of *rbcL* coding sequence

Table A3. GenBank accession data for taxa included in the Asterales-wide *rbcL* phylogenetic analysis.

Taxon	Accession number
Asterales	
Alseuosmiaceae	
<i>Crispiloba disperma</i> (S. Moore) Steenis	X87382
<i>Platyspermation crassifolium</i> Guillaumin	AJ419700
Argophyllaceae	
<i>Argophyllum</i> sp.	X87379
<i>Corokia cotoneaster</i> Raoul	L11221
Asteraceae	
<i>Achillea millefolium</i> L.	L13641
<i>Barnadesia caryophylla</i> (Vell.) S.F. Blake	L13859
<i>Bellis perennis</i> L.	AY395530
<i>Blennosperma nana</i> (Hook.) S. F. Blake	L13645
<i>Borrichia frutescens</i> DC.	AF119187
<i>Chromolaena</i> sp.	L13640
<i>Coreopsis grandiflora</i> Hogg	L13642
<i>Dasyphyllum dicanthoides</i> (Less.) Cabrera	L13863
<i>Dimorphotheca pluvialis</i> L.	L13636
<i>Eremothamnus marlothianus</i> O. Hoffm.	X89516
<i>Eupatorium atrorubens</i> Nicholson	L13649
<i>Felicia bergeriana</i> A. Zahlbr.	L13639
<i>Gerbera jamesonii</i> Bolus	L13643
<i>Helianthus annuus</i> L.	L13929
<i>Senecio mikanioides</i> Walp.	L13933
<i>Tagetes erecta</i> L.	L13637
<i>Tragopogon pratensis</i> L.	AY395563
<i>Vernonia mespilifolia</i> Less.	L13646
Calyceraceae	
<i>Acicarpha tribuloides</i> Juss.	X87376
<i>Boopis anthemoides</i> Juss.	L13860
Campanulaceae	
<i>Adenophora confusa</i> Nannf.	AY655145
<i>Asyneuma virgatum</i> Bornm.	AY655146
<i>Brighamia insignis</i> A. Gray	AF042664
<i>Campanula ramosissima</i> Sibth. & Sm.	L13861
<i>Centropogon gutierrezii</i> E. Wimmer	AF042658
<i>Clermontia kakeana</i> Meyen	L18789
<i>Codonopsis viridis</i> Wall.	AY655148
<i>Cyananthus lobatus</i> Wall. ex Benth.	AY655149
<i>Cyanea coriacea</i> (A. Gray) Hillebr.	AF042662
<i>Cyphia rogersii</i> S. Moore	AJ419698
<i>Cyphocarpus rigescens</i> Miers	L18792
<i>Delissea rhytidosperma</i> H. Mann	AF042663

<i>Dialypetalum</i> sp.	AJ318991
<i>Isotoma axillaris</i> Lindl.	DQ268874, DQ268875
<i>Jasione heldreichii</i> Boiss. & Orph.	AY655151
<i>Legousia falcate</i> Fritsch	AY655152
<i>Lobelia cardinalis</i> L.	AF042659
<i>Lobelia erinus</i> L.	L13930
<i>Lobelia nicotianaeefolia</i> Heyne	AF042660
<i>Lobelia vivaldii</i> Lammers & Proctor	DQ268873
<i>Merciera tenuifolia</i> A. DC.	AY655153
<i>Musschia aurea</i> Dum.	AY655154
<i>Nemacladus ramosissimus</i> Nutt.	L18791
<i>Petromarula pinnata</i> A. DC.	AY655155
<i>Platycodon grandiflorum</i> A. DC.	AY655156
<i>Pratia borneensis</i> Hemsl.	AF042665
<i>Prismatocarpus diffusus</i> A. DC.	AY655157
<i>Pseudonemacladus oppositifolius</i> (B.L. Rob.) McVaugh	AJ318992
<i>Roella ciliata</i> L.	AY655158
<i>Symphyandra hofmanni</i> Pant.	AY655159
<i>Trachelium caeruleum</i> L.	L18793
<i>Triodanis perfoliata</i> L. Nieuwl.	AY655160
<i>Wahlenbergia gloriosa</i> Lothian	AY655161

Donatiaceae

<i>Donatia novae-zelandiae</i> Hook.f.	AJ225058
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Goodeniaceae

<i>Goodenia ovata</i> Sm.	X87386
<i>Scaevola frutescens</i> Krause	L13932
<i>Selliera radicans</i> Cav.	X87395
<i>Velleia paradoxa</i> R.Br.	X87396
<i>Verreauxia reinwardtii</i> Benth.	X87397

Menyanthaceae

<i>Nymphoides peltata</i> Kuntze	X87392
<i>Villarsia calthifolia</i> F. Muell.	L11685

Pentaphragmataceae

<i>Pentaphragma ellipiticum</i> Poulsen	L18794
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Phellinaceae

<i>Phelline lucida</i> Vieill. ex Baill.	AJ238347
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Rousseaceae

<i>Abrophyllum ornans</i> Hook.f.	AF299090
<i>Cuttsia viburnea</i> F. Muell.	Y08462
<i>Rousea simplex</i> Sm.	AF084477

Stylidiaceae

<i>Forstera bidwillii</i> Hook.f.	AJ225055
<i>Levenhookia leptantha</i> Benth.	AJ225051
<i>Oreostylidium subulatum</i> Berggr.	AJ225057
<i>Phyllachne uliginosa</i> J.R. Forst. & G. Forst.	AF307929
<i>Stylium emarginatum</i> Sond.	AJ225052

OTHER ASTERIDS:

Apiales

Apiaceae		
<i>Apium graveolens</i> L.		L01885/L11165
Araliaceae		
<i>Aralia spinosa</i> L.		L11166
Griseliniaeae		
<i>Griselinia littoralis</i> (Raoul) Raoul		AF307916
Pittosporaceae		
<i>Pittosporum tobira</i> Dryand.		U50261

Aquifoliales

Aquifoliaceae		
<i>Ilex mitis</i> (L.) Radlk.		X98730
Cardiopteridaceae		
<i>Cardiopteris quinqueloba</i> Hassk.		AJ402936
Helwingiaceae		
<i>Helwingia japonica</i> (Thunb.) Dietr.		L11226

Cornales

Cornaceae		
<i>Cornus mas</i> L.		L11216
Grubbiaceae		
<i>Grubbia tomentosa</i> (thunb. Harms.		Z83141
Loasaceae		
<i>Loasa loxensis</i> Kunth		U17876

Dipsacales

Adoxaceae		
<i>Sambucus caerulea</i> Raf.		AJ420867
<i>Viburnum rhytidophyllum</i> Hemsl.		X87398
Caprifoliaceae		
<i>Lonicera orientalis</i> Lam.		X87389
<i>Symporicarpos orbiculatus</i> Moench		AF446934

Ericacales

Actinidiaceae		
<i>Actinidia chinensis</i> Planch.		L01882

Clethraceae		
<i>Clethra alnifolia</i> L.		L12609
Pentaphylaceae		
<i>Pentaphylax euryoides</i> Gardner & Champ.		AJ428891
Roridulaceae		
<i>Roridula gorgonias</i> Planch.		L01950
Theaceae		
<i>Sladenia celastrifolia</i> Kurz		AJ403004
Ternstroemiaceae		
<i>Ternstroemeria stahlii</i> Krug & Urban		Z80211

Unplaced to order under APG II

Bruniaceae		
<i>Berzelia lanuginosa</i> Brongn.		L14391
Escalloniaceae		
<i>Escallonia illinita</i> C. Presl.		AJ419694
Quintiniaceae		
<i>Quintinia verdonii</i> F. Muell		AF299092

ROSID OUTGROUP

Brassicales

Brassicaceae		
<i>Arabidopsis thaliana</i> (L.) Heynh.		AP999423

Table A4. Elevational occurrence, corolla tube length, and geographic distribution of individual species of *Cyanea* (see text for sources).

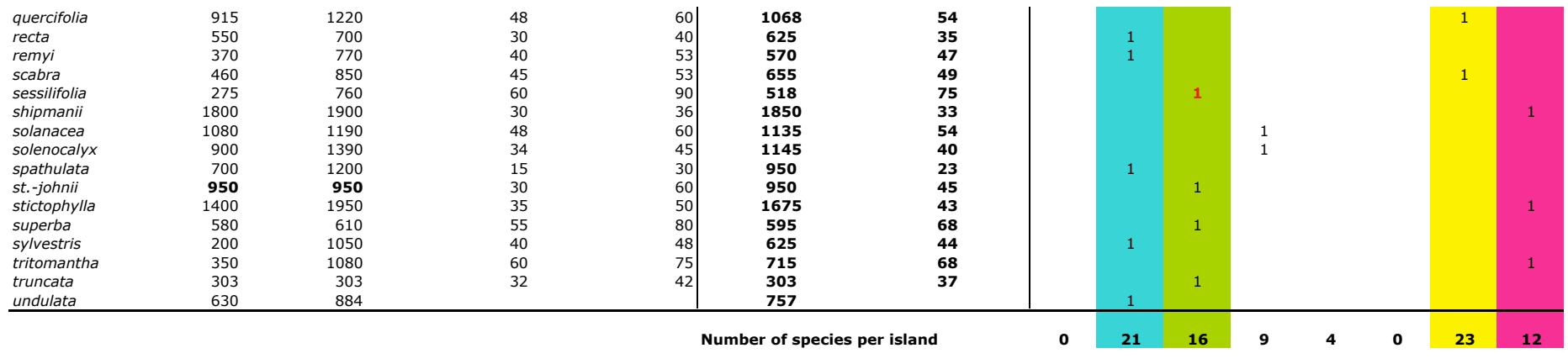


Table A5. Age, area, and elevation of the eight major Hawaiian Islands, and tabulation of the number of species from each endemic genus or section of the Hawaiian lobeliads present on each island.

	Ni`ihau	Kaua`i	O`ahu	Moloka`i	Maui	Lana`i	Kaho`olawe	Hawai`i
Geographic data:								
Age (My)	5.2	4.7	3.0	2.0	1.5	1.5	1.2	0.6
Area (km ²)	189	1624	1574	676	1887	361	116	10458
Maximum elevation (m)	390	1598	1225	1813	3055	1027	450	4205
Species present:								
<i>Cyanea</i>	0	21	16	9	23	4	0	12
<i>Clermontia</i>	0	1	4	5	10	4	0	11
<i>Delissea</i>	0	3	5	0	1	1	0	1
<i>Brighamia</i>	1	1	0	1	0	0	0	0
<i>Trematolobelia</i>	0	1	2	1	1	1	0	2
<i>Lobelia</i> sect. <i>Revolutella</i>	1	2	4	2	3	1	0	1
<i>Lobelia</i> sect. <i>Galeatella</i>	0	2	1	1	1	0	0	0
Total	2	31	32	19	39	11	0	27

Table A6. Observed vs. predicted numbers of species of *Cyanea* on each of the eight major Hawaiian islands. Model 1 (all islands, based on adjusted island elevation ϵ only): $S = 6.39 \times 10^{-4} \times \epsilon^{1.38} - 1$ ($r^2 = 0.89$, $P < 0.01$ for 6 d.f.). Model 2 (all islands except Hawai`i based on adjusted elevation ϵ and island area A): $\ln(1+S) = 0.620 \ln \epsilon + 0.761 \ln A - 7.12$ ($r^2 = 0.995$, $P < 0.01$ for each variable separately, $P < 5 \times 10^{-5}$ for combined equation, 5 d.f.; island age discarded in backwards-elimination multiple regression).

Island	Number of <i>Cyanea</i> species:		
	Observed	Expected, Model 1	Expected, Model 2
Ni`ihau	0	-0.1	0.1
Kaua`i	21	12.7	19.0
O`ahu	16	8.0	15.1
Moloka`i	9	15.7	10.2
Maui	23	18.4	25.2
Lana`i	4	5.7	3.6
Kaho`olawe	0	0.3	-0.1
Hawai`i	12	18.4	95.6